

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/937, 779 A
Source: IFW16
Date Processed by STIC: 11/18/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/937,779 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not** exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your subsequent submission is saved in **ASCII text**.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005

TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt

Output Set: N:\CRF4\11182005\I937779A.raw

3 <110> APPLICANT: Dahlqvist, Anders
 4 Stahl, Ulf
 5 Lenman, Marit
 6 Banas, Antoni
 7 Ronne, Hans
 8 Stymne, Sten

10 <120> TITLE OF INVENTION: PROCESSES FOR PRODUCING TRIACYLGLYCEROL USING GENES THAT
 ENCODE
 11 PHOSPHOLIPID:DIACYLGLYCEROL ACYLTRANSFERASES
 13 <130> FILE REFERENCE: BASFnae337799PCT1-15
 15 <140> CURRENT APPLICATION NUMBER: US 09/937779A

C--> 17 <141> CURRENT FILING DATE: 2002-07-02
 17 <150> PRIOR APPLICATION NUMBER: PCT / EP 00 / 02701
 18 <151> PRIOR FILING DATE: 2000-03-23
 20 <160> NUMBER OF SEQ ID NOS: 32
 22 <170> SOFTWARE: PatentIn Ver. 3.3

Does Not Comply
 Corrected Diskette Needed
 (pg - 1-17)

ERRORED SEQUENCES

335 <210> SEQ ID NO: 3
 336 <211> LENGTH: 2312
 E--> 337 <212> TYPE: genomic DNA
 338 <213> ORGANISM: Schizosaccharomyces pombe
 340 <400> SEQUENCE: 3

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 342 gacttaccaa attcaaagaa accaactcgc gctttgagtg agcaaccttc agcgtccgaa 120
 343 acacaatctg tttcaaataa atcaagaaaa tctaaatttg gaaaaagatt gaattttata 180
 344 ttgggcgcta ttttgggaat atgcggtgct ttttttttcg ctggttgaga cgacaatgct 240
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 347 aagccttcgc agtctcctag cggaaatgaa gttcaagttg gtcttgatat gtacaatgag 420
 348 ggatatcgaa gtgaccatcc tgttattatg gttcctggtg ttatcagctc aggattagaa 480
 349 agttggtcgt ttaataattg ctcgattcct tacttttagga aacgtctttg gggtagctgg 540
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 351 aaaaaaaccg gcttgatcc gaagggaatt aagctgctgag cagctcaggg gtttgaagca 660
 352 gctgattttt ttatcacggg ctattggatt tggagtaaag taattgaaaa ccttgctgca 720
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 357 gatcatattg aagcatttat aaatgtgagt ctcgatggtt gtttgactac gtttctaact 1020
 358 tttgaataga tatcgggatc tttgattgga gcacccaaaa cagtggcagc gcttttatcg 1080
 359 ggtgaaatga aagatacagg tattgtaatt acattaaaca tgttaatat taatttttgc 1140

Invalid <212> Response
 per 1.823 of Seq. Rules

Use "DNA" as response
 and explain any modification

in <220-223>
 Section.

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362 caaaaataca aatgtgctct actttttcta acttttaata gagagccatg atggttcgca 1320
363 ctatgggagg agttagttct atgcttcta aaggaggcga tgttgatgg ggaaatgcca 1380
364 gttgggtaag aaatatgtgc tgttaatttt ttattaatat ttaggctcca gatgatctta 1440
365 atcaaacaaa tttttccaat ggtgcaatta ttcgatatag agaagacatt gataaggacc 1500
366 acgatgaatt tgacatagat gatgcattac aattttttaa aaatgttaca gatgacgatt 1560
367 ttaaagtcac gctagcgaaa aattattccc acggtcttgc ttggactgaa aaagaagtgt 1620
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371 ggggcaacct gtcattgatt cctcggttaa tgatggaaca aaagttgaaa atgtgagaga 1860
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376 aaatgtatgt tcattttacc ttacaaattt ctattactaa ctcttgaaat aaggaaatta 2160
377 ttttaaaagt ttcacagggc catggtgact cggtaacaaa ccgttatata tcagatatcc 2220
378 agtacggaca taagttttgt agattgcaat taactaacta accgaacagg gaaataataa 2280
379 atgagataaa tctcgataaa cctagaaatt aa 2312

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382 <210> SEQ ID NO: 4

383 <211> LENGTH: 3685

E--> 384 <212> TYPE: genomic DNA → same error

385 <213> ORGANISM: Arabidopsis thaliana

387 <400> SEQUENCE: 4

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389 gtggtgcacg atgaggattc gcaaaagaaa ccacacgaat cttccaaatc ccaccataag 120
390 aaatcgaacg gaggaggga gtggtcgtgc atcgattctt gttgttggtt cattgggtgt 180
391 gtgtgtgtaa cctggtggtt tcttctcttc ctttacaacg caatgcctgc gagcttccct 240
392 cagtatgtaa cggagcgaat cacgggtcct ttgcctgacc cgcccggtgt taagctcaaa 300
393 aaagaaggtc ttaaggcgaa acatcctggt gtcttcattc ctgggattgt caccgggtggg 360
394 ctcgagcttt gggaaggcaa acaatgcgct gatggtttat tttagaaaacg tttgtggggg 420
395 ggaacttttg gtgaagtcta caaaagggtga gctcaacaat tctcactctt cctttatatt 480
396 gggattttgga ttggatctga tgagatcacg cacttgttgc ttcttcaaca tcaactaaac 540
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399 tggactattt ctgtttgatt gttaaactta ggatataaaa tagctgcctt ggaatttcaa 720
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406 cctcccgaac ctgctatgga tatattaaaa aaaaagtgtt ttgtgggttg catctttggt 1140
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TIME: 10:08:48

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Output Set: N:\CRF4\11182005\I937779A.raw

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414 cttaaatatg tttcatgttg aattaatagg tacgtgatca gactcttagc cgtatgaaaa 1620
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419 ttgcagttgc caggatttga atatctgctt atacttttga tgatcagaac cttggctctg 1920
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421 ctgacattgg ttgattattt ttgctgctta tgtaactgaa actctcttga gattagacaa 2040
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423 taacatttgt catactgtct tttggagggc attgaatttt gctatggaaa gcgctggagc 2160
424 ttccatgctt gcattcttta ccaattagcg ttattctgct tctttcaatt ttcttgata 2220
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447 tgcccatggt gatatcatgg gaaactttgc tttgatcgaa gatatcatga gggttgccgc 3600
448 cggaggtaac gggctctgata taggacatga ccaggtccac tctggcatat ttgaatggtc 3660
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E-->

452 <210> SEQ ID NO: 5

453 <211> LENGTH: 2427

454 <212> TYPE: CDNA

455 <213> ORGANISM: Arabidopsis thaliana

457 <400> SEQUENCE: 5

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460 tgccccttat tcatcggaag aagccgacgg agaaaccatc gacgccgcca tctgaagagg 180
461 tgggtgcacga tgaggattcg caaaagaaac cacacgaatc ttccaaatcc caccataaga 240
462 aatcgaacgg aggaggaag tggctcgtgca tcgattcttg ttggttggtt attgggtgtg 300
463 tgtgtgtaac ctggtggttt cttctcttcc tttacaacgc aatgcctgag agcttccctc 360

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RAW SEQUENCE LISTING

DATE: 11/18/2005

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TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt

Output Set: N:\CRF4\11182005\I937779A.raw

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465 aaagaaggtc ttaaggcgaa acatcctgtt gtcttcattc ctgggattgt caccggtggg 480
466 ctcgagcttt gggaaggcaa acaatgcgct gatggtttat ttagaaaacg tttgtgggg 540
467 ggaacttttg gtgaagtcta caaaaggcct ctatgttggg tggaaacacat gtcacttgac 600
468 aatgaaactg ggttggattc agctggtatt agagtctgag ctgtatcagg actcgtggct 660
469 gctgactact ttgtcctcctg ctactttgtc tgggcagtgc tgattgctaa ccttgccat 720
470 attggatatg aagagaaaaa tatgtacatg gctgcatatg actggcggct ttcgtttcag 780
471 aacacagagg tacgtgatca gactccttagc cgtatgaaaa gtaatataga gttgatggtt 840
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473 ctacatttta tgaagtgggt tgaggcacca gctcctctgg gtggcggggg tgggccagat 960
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475 aaagctgttg cagggccttt ctctgctgaa gcaaaggatg ttgcagttgc cagagcgatt 1080
476 gccccaggat tcttagacac cgatatattt agacttcaga ccttgccagca tgtaatgaga 1140
477 atgacacgca catgggactc aacaatgtct atgttaccga agggagggtga cacgatatgg 1200
478 ggcgggcttg attggtcacc ggagaaaaggc cacacctgtt gtgggaaaaa gcaaaagaac 1260
479 aacgaaactt gtggtgaagc aggtgaaaac ggagtttcca agaaaagtcc tgtaaactat 1320
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483 tacactgctg gtgaagctat agatctacta cattatgttg ctctaagat gatggcgcgt 1560
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489 gccgggtaca tgtgtgcaaa agcgtggcgt ggcaagacaa gattcaacct ttcgggaatc 1920
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496 ctcaatacct ctttaatat cttattgaat gtaaattata caatcctatc taatgtttga 2340
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640 <213> ORGANISM: Zea mays
642 <220> FEATURE:
643 <221> NAME/KEY: CDS
644 <222> LOCATION: (1)..(402)
646 <400> SEQUENCE: 7
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648 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
649 1 5 10 15
651 gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga 96
652 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
653 20 25 30

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See page 17 for Error Explanation

Same Error, See page 5

RAW SEQUENCE LISTING

DATE: 11/18/2005

PATENT APPLICATION: US/09/937,779A

TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt

Output Set : N:\CRF4\11182005\I937779A.raw

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657      35      40      45
659 aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc 192
660 Arg Glu Tyr Ser His Ser Pro Ser Thr Leu Leu Glu Gly Arg Gly
661      50      55      60
663 acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240
664 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
665 65      70      75      80
667 gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt 288
668 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
669      85      90      95
671 ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa 336
672 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
673      100      105      110
675 ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att 384
676 Leu Lys Leu
677      115
679 gcg ttc caa agt gtc ctg cctgagtgc actctggatt ttgcttaaatt 432
681 attgtaattt ttcacgttc attcgtccct ttgtcaaatt tacatttgac aggacgcaa 492
683 tgcgatacga tttgtaccg ctattttcag cattgtatat taaactgtac aggtgtaagt 552
W--> 685 tgcatttgcc agctgaaatt gtgtagtcgt tttctttacg atttaataat aagtggcgga 612
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717 <211> LENGTH: 616
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719 <213> ORGANISM: Neurospora crassa
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727 aaatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcatgaac 360
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732 aaaaaaaaaa aaaaaa 616
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736 <211> LENGTH: 1562
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744 agcagctggt tatatccgat tcataagaag agtgggtggat ggtttaggct atggttcgat 240
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747 ggttcgacca aatcacttct atacctcgac cctcgtctcc ggtagtact ttccaagata 420
748 tatcattttg ggacatttgc ataatgaaca aaatagacat aaatttgggg gattattgtt 480
749 atatcaatat ccatttatat gctagtcggt aatgtgagtg ttatgttagt atagttaatg 540
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751 ctatgtcatg agaattataa ggacactatg taaatgtagc ttaataataa ggtttgattt 660
752 gcagagatgc cacatcttac atggaacatt tggtgaaagc tctagagaaa aaatgcgggt 720
753 atgttaacga ccaaacctac ctaggagctc catatgattt caggtagcgc ctggctgctt 780
754 cgggccaccc gtcccgtgta gcctcacagt tcctacaaga cctcaaacia ttggtggaaa 840
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762 agctgatgac tccgggagtg ccagtcactt gcataatagg gagaggagtt gatacaccgg 1320
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765 tagagattga tggagtttcg catacatcta tacttaaaga cgagatcgca cttaaagaga 1500
766 ttatgaagca gatttcaatt attaatatg aattagccaa tgttaatgcc gtcaatgaat 1560
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773 <213> ORGANISM: Arabidopsis thaliana

775 <400> SEQUENCE: 11

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778 ctatcgggta taatcattcc gggatttgcg tcgacgcagc tacgagcgtg gtcgatcctt 180
779 gactgtccat acactccgtt ggacttcaat ccgctcgacc tcgtatggct agacaccact 240
780 aagggtccgt atcttcattt ccttcgctcc ttattctgtc ggtcagatca cttgttgatg 300
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787 taatcaaaca gaccatcccg agtgtaagtc acggcctgac agtgggtctt cagccatcac 720
788 agaattggat ccagggtaca taacaggtag tttcggattt ttctttcttt tgagttttct 780
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807 aggggtgataa cacattctgg acgcattttt ctgggggtgc tgcaaagaaa gataagcgcg 1920
808 tataccactg tgatgaagag gaatatcaat caaaatatc tggctggccg acaaattatta 1980
809 ttaacattga aattccttcc actagcgggt agactctgta tatgcaactg taacactaac 2040
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Same Error

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 2211 taacatttgt cactactgtt tttggagggc attgaatttt gctatggaaa gcgctggagc 2160
 2212 ttccatgctt gcattcttta ccaattagcg ttattctgct tctttcaatt ttcttgata 2220
 2213 tgcactctat gtcttttatt tcttcttaat taaagactcg ttggattagt tgctctatta 2280

RAW SEQUENCE LISTING

DATE: 11/18/2005

PATENT APPLICATION: US/09/937,779A

TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt

Output Set : N:\CRF4\11182005\I937779A.raw

```

2214 gtcacttggt tccttaatat agaactttac tttcttcgaa aattgcagag cgattgcccc 2340
2215 aggattctta gacaccgata tatttagact tcagaccttg cagcatgtaa tgagaatgac 2400
2216 acgcacatgg gactcaacaa tgtctatggt accgaaggga ggtgacacga tatggggcgg 2460
2217 gcttgattgg tcaccggaga aaggccacac ctggttgagg aaaaagcaaa agaacaacga 2520
2218 aacttggtgg gaagcagggtg aaaacggagt ttccaagaaa agtcctgtta actatggaag 2580
2219 gatgatattct tttgggaaag aagtagcaga ggctgcgcca tctgagatta ataattatga 2640
2220 ttttcgagta aggacatata aatcataata aaccttgtag attttgtgat tgtatgatga 2700
2221 atatctgtac attttatctg gtgaagggtg ctgtcaaagg tcagagtatc ccaaatacaca 2760
2222 cctgtcgtga cgtgtggaca gaggaccatg acatgggaat tgcctgggatc aaagctatcg 2820
2223 ctgagtataa ggtctacact gctggtgaag ctatagatct actacattat gttgctccta 2880
2224 agatgatggc gcgtggtgcc gctcatttct cttatggaat tgcctgatgat ttggatgaca 2940
2225 ccaagtatca agatcccaaa tactggtcaa atccggttaga gacaaagtaa gtgatttctt 3000
2226 gattccaact gtatccttcg tctgatgca ttatcagctt tttgttttc ggtcttggtg 3060
2227 gatatggttt tcagctcaaa gcttacaagg ctgtttctga gcctttctca aaaaggcttg 3120
2228 ctacagtaata ttgaggtgct aaagttgata catgtgactc ttgcttataa atcctccgtt 3180
2229 tgggttggtc tgctttttca gattaccgaa tgctcctgag atggaaatct actcattata 3240
2230 cggagtgagg ataccaacgg aacgagcata cgtatacaag cttaccagct cccccgacag 3300
2231 ttgcatcccc tttcagatat tcaattctgc tcacgaggag gacgaagata gctgtctgaa 3360
2232 agcaggagtt tacaatgtgg atggggatga aacagtaccc gtcttaagtg ccgggtacat 3420
2233 gtgtgcaaaa gcgtggcgtg gcaagacaag attcaaccct tccggaatca agacttatat 3480
2234 aagagaatac aatcactctc cgccggctaa cctgttgga gggcgcgagg cgcagagtgg 3540
2235 tgcccatggt gatatcatgg gaaactttgc tttgatcgaa gatatcatga ggggtgcccgc 3600
2236 cggaggtaac gggctctgata taggacatga ccaggtccac tctggcatat ttgaatgggc 3660
2237 ggagcgtatt gacctgaagc tgtga 3685

```

2240 <210> SEQ ID NO: 25

2241 <211> LENGTH: 402

E--> 2242 <212> TYPE: CDNA → *same error*

2243 <213> ORGANISM: Arabidopsis thaliana

2245 <220> FEATURE:

2246 <221> NAME/KEY: CDS

2247 <222> LOCATION: (120)..(401)

2249 <400> SEQUENCE: 25

2250 agaaacagct ctttgtctct ctcgactgat ctaacaatcc ctaatctgtg ttctaaattc 60

2252 ctggacgaga tttgacaaaag tccgtatagc ttaacctggg ttaatttcaa gtgacagat 119

2254 atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg 167

2255 Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro

2256 1 5 10 15

2258 cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215

2259 Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His

2260 20 25 30

W--> 2262 gaa tct tcc aaa tcc cac cat aag gaa tcg aac gga gga ggg aag tgg 263

W--> 2263 Glu Ser Ser Lys Ser His His Lys Xaa Ser Asn Gly Gly Gly Lys Trp

2264 35 40 45

2266 tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc 311

2267 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr

2268 50 55 60

2270 tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct 359

2271 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro

2272 65 70 75 80

see page 17

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Input Set : N:\RJAVED\09937779.txt

Output Set: N:\CRF4\11182005\I937779A.raw

W--> 2274 cag tat gta acg gag ccg aat cac gng tcc ttt gcc tta ccc g 402
W--> 2275 Gln Tyr Val Thr Glu Pro Asn His Xaa Ser Phe Ala Leu Pro
2276 85 90

2279 <210> SEQ ID NO: 26
2280 <211> LENGTH: 643

E--> 2281 <212> TYPE: CDNA → Same Error
2282 <213> ORGANISM: Zea mays
2284 <220> FEATURE:
2285 <221> NAME/KEY: CDS
2286 <222> LOCATION: (1)..(402)
2288 <400> SEQUENCE: 26

2290 cgg gag aaa ata gct gct ttg aag ggg ggt gtt tac tta gcc gat ggt 48
2291 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
2292 1 5 10 15
2294 gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga 96
2295 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
2296 20 25 30
2298 tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144
2299 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
2300 35 40 45
2302 aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc 192
2303 Arg Glu Tyr Ser His Ser Pro Ser Thr Leu Leu Glu Gly Arg Gly
2304 50 55 60
2306 acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240
2307 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
2308 65 70 75 80
2310 gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt 288
2311 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
2312 85 90 95
2314 ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa 336
2315 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
2316 100 105 110
2318 ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att 384
2319 Leu Lys Leu
2320 115
2322 gcg ttc caa agt gtc ctg cctgagtga actctggatt ttgcttaaat 432
2324 attgtaattt ttcacgcttc attcgtccct ttgtcaaatt tacatttgac aggacgccaa 492
2326 tgcgatacga tggtgtaccg ctattttcag cattgtatat taaactgtac aggtgtaagt 552
W--> 2328 tgcatttgcc agctgaaatt gtgtagtcgt tttctttacg atttaataat aagtggcgga 612
W--> 2330 gcagtgcgcc aagcnaaaaa aaaaaaaaaa a 643

2333 <210> SEQ ID NO: 27
2334 <211> LENGTH: 115
2335 <212> TYPE: PRT
2336 <213> ORGANISM: Zea mays

E--> 2338 <400> SEQUENCE: (30) → 27
2339 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
2340 1 5 10 15
2341 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
2342 20 25 30

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TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt

Output Set: N:\CRF4\11182005\I937779A.raw

2343 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 2344 35 40 45
 2345 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 2346 50 55 60
 2347 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 2348 65 70 75 80
 2349 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 2350 85 90 95
 2351 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 2352 100 105 110
 2353 Leu Lys Leu
 2354 115

2357 <210> SEQ ID NO: 28
 2358 <211> LENGTH: 516
 E--> 2359 <212> TYPE: CDNA *same error*
 2360 <213> ORGANISM: Neurospora crassa
 2362 <400> SEQUENCE: 28
 E--> 2363 ggtggcgaag acgagggcgg aagttggagg ctaacgagaa tgacnctcgg agatggatct 60
 E--> 2364 accctctaga gacacgacta c~~ont~~ttgcacc cagcctcaag g~~tn~~ta~~on~~tt t~~nt~~atgggta 120
 2365 ggaagccgac ggagcgagcc tacatctatc tggcgcccga tcccgggacg acaacgcac 180
 E--> 2366 tttagatgac gatcgatagc actttgact~~n~~ aggggcacat tgaccacggt gtgattttgg 240
 2367 gcgaaggcga tggcacagtg aaccttatga gtttgggta cctgtgcaat aaggggtgga 300
 2368 aaatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcátgaac 360
 2369 cagaacggtt caatccgaga ggagggccga atacggcgga cttaaataatg tagaaaagg 420
 2370 tgaaatttat gaagagtaat taaatacggc acataggtta ctcaatagta tgactaatta 480
 2371 aaaaaaaatt ttttttctaa aaaaaaaaaa aaaaaa 516
 2374 <210> SEQ ID NO: 29
 2375 <211> LENGTH: 1562
 E--> 2376 <212> TYPE: genomic DNA *same error*
 2377 <213> ORGANISM: Arabidopsis thaliana
 2379 <400> SEQUENCE: 29
 2380 atgaaaaaaaa tatcttcaca ttattcggta gtcatagcga tactcgttgt ggtgacgatg 60
 2381 acctcgatgt gtcaagctgt gggtagcaac gtgtaccctt tgattctggt tccaggaaac 120
 2382 ggaggttaacc agctagaggt acggctggac agagaataca agccaagtag tgtctggtgt 180
 2383 agcagctggt tatatccgat tcataagaag agtggtggat ggtttaggct atggttcgat 240
 2384 gcagcagtgt tattgtctcc cttcaccagg tgcttcagcg atcgaatgat gttgtactat 300
 2385 gaccctgatt tggatgatta ccaaaatgct cctggtgtcc aaaccgggt tccctatttc 360
 2386 ggttcgacca aatcacttct atacctcgac cctcgtctcc ggtagtagt tccaagata 420
 2387 tatcattttg ggacatttgc ataatagaaca aaatagacat aaatttgggg gattattggt 480
 2388 atatcaatat ccatttatat gctagtcggt aatgtgagtg ttatgttagt atagttaatg 540
 2389 tgagtgttat gtgattttcc attttaaatg aagctagaaa gttgtcgttt aataatggtg 600
 2390 ctatgtcatg agaattataa ggacactatg taaatgtagc ttaataataa ggtttgattt 660
 2391 gcagagatgc cacatcttac atggaacatt tgggtgaaagc tctagagaaa aaatgcccgt 720
 2392 atgttaacga ccaaaccatc ctaggagctc catatgattt caggtagcgc ctggctgctt 780
 2393 cgggccaccc gtcccggtga gcctcacagt tectacaaga cctcaaaca ttggtggaaa 840
 2394 aaactagcag cgagaacgaa ggaaagccag tgatactcct ctcccatagc ctaggaggac 900
 2395 ttttcgtcct ccatttcctc aaccgtacca ccccttcctg gcgccgcaag tacatcaaac 960
 2396 actttgttgc actcgtcgcg ccatggggtg ggacgatctc tcagatgaag acatttgctt 1020
 2397 ctggcaacac actcgtgtgc cctttagtta accctttgct ggtcagacgg catcagagga 1080

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Input Set : N:\RJAVED\09937779.txt

Output Set: N:\CRF4\11182005\I937779A.raw

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2398 cctccgagag taaccaatgg ctacttccat ctaccaaagt gtttcacgac agaactaaac 1140
2399 cgcttgctcg aactccccag gttaactaca cagcttacga gatggatcgg ttttttgcag 1200
2400 acattggatt ctcacaagga gttgtgcctt acaagacaag agtggtgcct ttaacagagg 1260
2401 agctgatgac tccgggagtg ccagtcactt gcataatgg gagaggagtt gatacacagg 1320
2402 aggttttggat gtatggaaaa ggaggattcg ataagcaacc agagattaag tatggagatg 1380
2403 gagatgggac ggttaatttg gcgagcttag cagctttgaa agtcgatagc ttgaacaccg 1440
2404 tagagattga tggagtttgc catacatcta tacttaaaga cgagatcgca cttaaagaga 1500
2405 ttatgaagca gatttcaatt attaattatg aattagccaa tgtaaatgcc gtcaatgaat 1560
2406 ga 1562

```

2409 <210> SEQ ID NO: 30

2410 <211> LENGTH: 3896

E--> 2411 <212> TYPE: genomic DNA

2412 <213> ORGANISM: Arabidopsis thaliana

2414 <400> SEQUENCE: 30

```

2415 atgggagcga attcgaaatc agtaacggct tccttcaccg tcatcgccgt ttttttcttg 60
2416 atttgcgggtg gccgaactgc ggtggaggat gagaccgagt ttcacggcga ctactcgaag 120
2417 ctatcgggta taatcattcc gggatttgcg tcgacgcagc tacgagcgtg gtcgatcctt 180
2418 gactgtccat acactccgtt ggacttcaat ccgctcgacc tcgtatggct agacaccact 240
2419 aagggtccgtg atcttcattt ccttcgctcc ttattctgtc ggtcgagtca cttgttgatg 300
2420 aattccaagc gaaatatagc aatgaagcat gtctcgtctc tcttattgat tcgttcatta 360
2421 gtcaacagtg acgcttttga atctgagttt agagctatat aaaacagctg actcggcgag 420
2422 tgtttcccat cgcttttggg tcgctaaatg tagcgcaatg aatgtgtaat tagtctgcgc 480
2423 tttttattca actagatctg caagtttttc agagtgtca atagtagtta gaaaatgtta 540
2424 ggtcatttta cttgtgcatt gtgattcttt tgggtgttgc ttactgatcg acgtgatgga 600
2425 tggtttacag cttctttctg ctgtcaactg ctggtttaag tgtatggtgc tagatcctta 660
2426 taatcaaaca gaccatcccg agtgtaagtc acggcctgac agtggtcttt cagccatcac 720
2427 agaattggat ccaggttaca taacaggtag tttcggattt ttctttcttt tgagttttct 780
2428 tcaatttgat atcatcttgt tgtgatataa tatggctaag ttcattaatt tgggtcaattt 840
2429 tcaggctctc tttctactgt ctggaaagag tggcttaagt ggtgtgttga gtttggata 900
2430 gaagcaaatg caattgtcgc tgttccatac gattggagat tgtcaccaac caaattggaa 960
2431 gagcgtgacc tttactttca caagctcaag ttagtcctta tcaggctaag gtcttttatc 1020
2432 ttctcttttt atgtaagata agctaagagc tctggctcgc ttcctttttg caggttgacc 1080
2433 tttgaaactg ctttaaaact ccgtggcggc ccttctatag tatttgccca ttcaatgggt 1140
2434 aataatgtct tcagatactt tctggaatgg ctgaggctag aaattgcacc aaaacattat 1200
2435 ttgaagtggc ttgatcagca tatccatgct tatttcgctg ttggtaccgg cctactatcc 1260
2436 ttaagttacc attttatttt ttctctaatt gggggagtta tgttgtgact tactggattg 1320
2437 agctcgatac ctgatttgtt gttgatttag gagctcctct tcttgggtct gttgaggcaa 1380
2438 tcaaatctac tctctctggg gtaacgtttg gccttcctgt ttctgaggtg acctctgact 1440
2439 tctctttagt ttttaagtagt tgatatcaac caggctttat aactcactgg attttccttt 1500
2440 tgaaagtatt acttttgtta attgaactgc tgtacgcgat atggtatctg tagatcttga 1560
2441 agtgctagtt atcaaagaac atattgtggg tagtatacct gtcagcggcc ttagctaata 1620
2442 caaccaaac acatgtacac tgatttagtt ttcagattat tatggtagac ttttaagttga 1680
2443 gaagaaactt tgactgaaat ctttttattt taataggcta tgatttgttt attgaaatca 1740
2444 tgtgacatat tgacatgcgc ttctcatgtt ttttgttggc aaggcttcag ggaactgctc 1800
2445 ggttgttgtc caattctttt gcgtcgtcat tgtggcttat gccattttca aagaattgca 1860
2446 aggggtgata cacattctgg acgcattttt ctgggggtgc tgcaaagaaa gataagcgcg 1920
2447 tataccactg tgatgaagag gaatatcaat caaaatattc tggctggccg acaaattatta 1980
2448 ttaacattga aattccttcc actagecggt agactctgta tatgcaactg taacactaac 2040
2449 aaaagtttca ccaagaatgt tcaactctcat atttcgttcc tttgatgtgt atccatcagt 2100

```

Same Error

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PATENT APPLICATION: US/09/937,779A

TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt

Output Set: N:\CRF4\11182005\I937779A.raw

```

2450 tacagaaaca gctctagtca acatgaccag catggaatgt ggccttccca cccttttgtc 2160
2451 tttcacagcc cgtgaactag cagatgggac tcttttcaaa gcaatagaag actatgaccc 2220
2452 agatagcaag aggatgttac accagttaaa gaagtacgta cctttctttg tgataagaaa 2280
2453 tattgctcat cgatcatcac ttgctggctt cttgtacgta aaattgtttt gtttaaactc 2340
2454 ctatatcaat gtgtcatatg ctttgtcttt cttactataa gaaacaagta taatcagaaa 2400
2455 ccttattatt gattatcagt tctctcctta tattatggaa tgtctttttc gtttacagtt 2460
2456 atgaatgcaa aaggggggat tttagttgat tgattctctc attctctagt ttgttttgac 2520
2457 taatagcgct aattttgttt ttctagcaaa tctttgtgaa ttatatataa catgctaact 2580
2458 ataactttca ggttgtatca tgatgacctt gtttttaate ctctgactcc ttgggagaga 2640
2459 ccacctataa aaaatgtatt ttgcatatat ggtgctcatc taaagacaga ggtatgatgc 2700
2460 attctcaata tcacattatg cgttgacttt gttattatat tccccatttg gtttgcaata 2760
2461 tctttttgaa ttatgattta tcttctccct tgcactttat gctattaagc gttaaaggta 2820
2462 ctaaagtgtat gaagctgtct gtcataaggtt ggttattact ttgccccagc tggcaaacct 2880
2463 tatcctgata attggatcat cacggatata atttatgaaa ctgaagggtc cctcgtgtca 2940
2464 aggtaatttt ccgcaatggc agaagtaaaa caggaaggca aagtcttctg tatcagtcta 3000
2465 gtggcatggt atctcagttg cataagcaaa ttattaaaca actaaaattt aagtactttt 3060
2466 ttatcattcc ttttgagctt agtggatgat cagtggctta aagtgggaag aggtgttgca 3120
2467 tgaaacatga cacttgtatc aaagataact agcaaaaaca aactaaccce tttctgaatt 3180
2468 tcatattatt aggagtagtc gtgcttttaa aaaatttgtt ttaagaaacc gaaaaactag 3240
2469 ttcatatcct gattgtgcaa tatctgcagg tctggaactg tgggtgatgg gaacgctgga 3300
2470 cctaatctg gggatgagac ggtaagctca gaagtgggtt ttgaaattat cttcttgcaa 3360
2471 actactgaag actaagataa tacttggctt tggaacactg cttgctatgt tctctagtac 3420
2472 actgcaatat tgactctccg ctacttttat tgattatgaa attgatctct tatagggtacc 3480
2473 ctatcattca ctctcttggg gcaagaattg gctcggacct aaagttaaca taacaatggc 3540
2474 tccccaggta ctctttttta gttctctacc ttatatagat caaactttta gtgtactttt 3600
2475 ctggttatgt gttgatttac ctccaatttg ttctttctaa aaatcatata tctctgtact 3660
2476 cctcaagaac ttgtattaat ctaaacgaga ttctcattgg gaaaataaaa caacagccag 3720
2477 aacacgatgg aagcgacgta catgtggaac taaatgttga tcatgagcat gggtcagaca 3780
2478 tcatagctaa catgacaaaa gcaccaaggg ttaagtacat aaccttttat gaagactctg 3840
2479 agagcattcc ggggaagaga accgcagtct gggagcttga taaaagtggt tattaa 3896

```

2482 <210> SEQ ID NO: 31

2483 <211> LENGTH: 709

E--> 2484 <212> TYPE: CDNA → Same Error

2485 <213> ORGANISM: tomato

2487 <400> SEQUENCE: 31

```

2488 ctggggccaa aagtgaacat aacaaggaca ccacagtcag agcatgatgt tcagatgtac 60
2489 aagtgcattc aaatatagag catcaacatg gtgaagatat cattcccaat atgacaaaagt 120
2490 tacctacaat gaagtacata acctattatg aggattctga aagttttcca gggacaagaa 180
2491 cagcagtttg ggagcttgat aaagcaaatc acaggaacat tgtcagatct ccagctttga 240
2492 tgcgggagct gtggcttgag atgtggcatg atattcatcc tgataaaaag tccaagtttg 300
2493 ttacaaaagg tgggtgtctga tctcactat tttctctat aaatgtttga gtttgtattg 360
2494 acattgtaag tattgcaaca aaaagcaaa cgtgggcttc tgagggatga ggactgctat 420
2495 tgggattacg ggaaagctcg atgtgcatgg gctgaacatt gtgaatacag gttagaatat 480
2496 tcaaattata ttttgcaaaa tattctcttt ttgtgtattt aggccacctt tccccgggtc 540
2497 caacgatgca gatatgtatt cggggatgtt cacctgggac agagttgcag attgaagagt 600
2498 tctacatctc acatcctgtc acactatgtg tgatatttaa gaaactttgt ttggcggaac 660
2499 aacaagtttg cacaacatt tgaagaagaa agcgaaatga ttcagagag 709

```

2502 <210> SEQ ID NO: 32

2503 <211> LENGTH: 7

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RAW SEQUENCE LISTING

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TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt

Output Set: N:\CRF4\11182005\I937779A.raw

2504 <212> TYPE: PRT
2505 <213> ORGANISM: Conserved Sequence
E--> 2507 <400> SEQUENCE: 7 32
E--> 2508 Phe Xaa Lys Trp Val Glu Ala
2509 1 5
2517 2/58
2518 BASF-NAE 33 77 / 99 PCT 12.09.2000
E--> 2520 1
2522 1/58
2523 09/937,779 OA July 13, 2005
E--> 2524 Dalquist et al.

Invalid Response.
<213> Can be either
Artificial, Unknown
or Genus Species.
Pls see Item #
10 on Error
Summary Sheet.

See page
Pls Delete.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/18/2005
PATENT APPLICATION: US/09/937,779A TIME: 10:08:49

Input Set : N:\RJAVED\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1

VARIABLE LOCATION SUMMARY

DATE: 11/18/2005

PATENT APPLICATION: US/09/937,779A

TIME: 10:08:49

Input Set : N:\RJAVED\09937779.txt

Output Set: N:\CRF4\11182005\I937779A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:5; N Pos. 2363

Seq#:7; N Pos. 601,627

Seq#:9; N Pos. 15,45,83,103,107,112,210

Seq#:25; N Pos. 240,385

Seq#:25; Xaa Pos. 41,89

Seq#:26; N Pos. 601,627

Seq#:28; N Pos. 15,45,83,103,107,112,210

Seq#:32; Xaa Pos. 2

Error explanation

VERIFICATION SUMMARY

DATE: 11/18/2005

PATENT APPLICATION: US/09/937,779A

TIME: 10:08:49

Input Set : N:\RJAVED\09937779.txt

Output Set: N:\CRF4\11182005\I937779A.raw

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:28 M:283 W: Missing Blank Line separator, <220> field identifier
 L:337 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:3
 L:384 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:4
 L:454 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:5
 L:497 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
 L:639 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:7
 L:685 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:7
 L:685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:552
 L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:612
 L:718 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:9
 L:722 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
 L:723 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
 L:725 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
 L:737 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:10
 L:772 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:11
 L:845 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:12
 L:2125 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:23
 L:2172 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:24
 L:2242 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:25
 L:2262 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:25
 L:2262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:215
 L:2263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:263
 L:2274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:359
 L:2275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:402
 L:2281 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:26
 L:2328 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:26
 L:2328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:552
 L:2330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:612
 L:2338 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:27 differs:30
 L:2359 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:28
 L:2363 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
 L:2364 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
 L:2366 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
 L:2376 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:29
 L:2411 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:30
 L:2484 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:31
 L:2507 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:7
 L:2508 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
 L:2520 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
 L:2524 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:2524 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:3
 L:2524 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:10 SEQ:32